Original article:

MUTATIONS IN THE SARS-COV-2 SPIKE PROTEIN MODULATE THE VIRUS AFFINITY TO THE HUMAN ACE2 RECEPTOR, AN *IN SILICO* ANALYSIS

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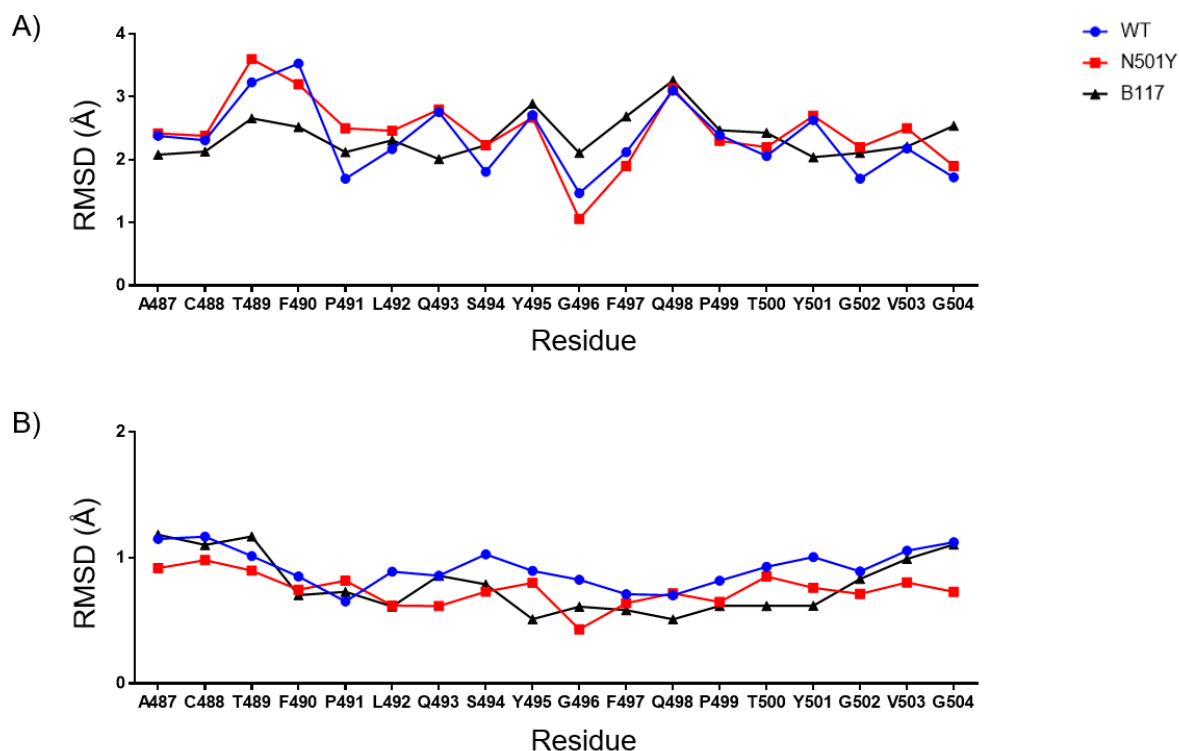E-mail: hrangel2006@gmail.com
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A)

B)

Supplementary Figure 1: The root-mean-square-deviation (RMSD) of the protein Cα atoms with the respect to the initial structure for the evaluated spike protein-ACE2 complex was obtained by molecular docking. **A**): The analysis performed with the VegaZZ software and **B**): The analysis performed with the CABS-Flex software.